SEQUENCE SEARCH SUMMARY

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 21, 2003, 16:22:11 ; Search time 4590 Seconds
                                      (without alignments)
                                      10793.368 Million cell updates/sec

Title: US-09-942-935-1
Perfect score: 1211
Sequence: 1 gacaccaatccacagatgca..........ccaggctttgaaaagggaat 1211

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   GenEmbl:*
                 1: gb_ba:*
                 2: gb_htg:*
                 3: gb_in:*
                 4: gb_om:*
                 5: gb_ov:*
                 6: gb_pat:*
                 7: gb_ph:*
                 8: gb_pl:*
                 9: gb_pr:*
                 10: gb_ro:*
                 11: gb_sts:*
                 12: gb_sy:*
                 13: gb_un:*
                 14: gb_vi:*
                 15: em_ba:*
                 16: em_fun:*
                 17: em_hum:*
                 18: em_in:*
                 19: em_mu:*
                 20: em_om:*
                 21: em_or:*
                 22: em_ov:*
                 23: em_pat:*
                 24: em_ph:*
                 25: em_pl:*
                 26: em_ro:*
                 27: em_sts:*

```
                    28:  em_un:*
                    29:  em_vi:*
                    30:  em_htg_hum:*
                    31:  em_htg_inv:*
                    32:  em_htg_other:*
                    33:  em_htg_mus:*
                    34:  em_htg_pln:*
                    35:  em_htg_rod:*
                    36:  em_htg_mam:*
                    37:  em_htg_vrt:*
                    38:  em_sy:*
                    39:  em_htgo_hum:*
                    40:  em_htgo_mus:*
                    41:  em_htgo_other:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID		Description
	1	1211	100.0	1211	6	AX394331	*WO 0218599 - Appl.*	AX394331 Sequence
	2	1211	100.0	309400	6	AX127153	*EP 1108790*	AX127153 Sequence
	3	1211	100.0	325651	1	AP005283	*GenBank AP005283*	AP005283 Corynebac
	4	603	49.8	603	6	AX123500	*EP fragment*	AX123500 Sequence
	5	603	49.8	603	6	BD165617	*JP fragment*	BD165617 Novel pol
c	6	449	37.1	1185	6	AX123502	*EP fragment*	AX123502 Sequence
c	7	449	37.1	1185	6	BD165619	*JP fragment*	BD165619 Novel pol
	8	243.6	20.1	87340	1	AP005224		AP005224 Corynebac
	9	197	16.3	951	6	AX123501		AX123501 Sequence
	10	197	16.3	951	6	BD165618		BD165618 Novel pol
	11	96.8	8.0	1775	1	AF023161		AF023161 Mycobacte
c	12	79.6	6.6	1443	6	AR227225		AR227225 Sequence
	13	79	6.5	1800	1	MLTRTRXHP		X87899 M.leprae TR
	14	79	6.5	40571	1	MSGDNAB		L39923 Mycobacteri
	15	79	6.5	269203	1	MLEPRTN10		AL583926 Mycobacte
	16	77.6	6.4	300956	1	AE016963		AE016963 Coxiella
	17	75	6.2	1529	1	MTTRTRXGN		X95798 M.tuberculo
	18	75	6.2	9882	1	AE007194		AE007194 Mycobacte
	19	75	6.2	10940	1	AE009169		AE009169 Agrobacte
	20	75	6.2	11381	1	MTV028		AL021426 Mycobacte
	21	75	6.2	12357	1	AE008135		AE008135 Agrobacte
c	22	75	6.2	35336	1	MSGY367		AD000008 Mycobacte
	23	73.4	6.1	278492	1	BX248347		BX248347 Mycobacte
c	24	72.8	6.0	7542	1	CBTRXB		X75627 C.burnetii
c	25	72.6	6.0	49617	6	AX067453		AX067453 Sequence
	26	71.8	5.9	2556	1	AF009622		AF009622 Listeria
c	27	71.8	5.9	324050	1	AL591983		AL591983 Listeria
c	28	71.8	5.9	349980	6	AX641672		AX641672 Sequence
	29	71	5.9	3075	6	AX064225		AX064225 Sequence
	30	71	5.9	3075	6	AX064311		AX064311 Sequence
	31	70.2	5.8	4900	1	AF418548		AF418548 Mycobacte
c	32	68.8	5.7	11790	1	AE011835		AE011835 Xanthomon
c	33	68.6	5.7	977	6	AX416278		AX416278 Sequence

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OM nucleic - nucleic search, using sw model

Run on: September 21, 2003, 16:21:16 ; Search time 390 Seconds
                                              (without alignments)
                                              8382.101 Million cell updates/sec

Title: US-09-942-935-1
Perfect score: 1211
Sequence: 1 gacaccaatccacagatgca..........ccaggctttgaaaagggaat 1211

Scoring table: IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   N_Geneseq_19Jun03:*
                  1: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
                  2: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
                  3: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
                  4: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
                  5: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
                  6: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
                  7: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
                  8: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
                  9: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
                  10: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*
                  11: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
                  12: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
                  13: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
                  14: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
                  15: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
                  16: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
                  17: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
                  18: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*
                  19: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
                  20: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
                  21: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
                  22: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
                  23: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
                  24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
                  25: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2003.DAT:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID		Description
	1	1211	100.0	1211	24	AAL42355	*Appl. WO*	Corynebacterium gl
	2	1211	100.0	309400	22	AAH68534	*EP 1108790*	C glutamicum codin
	3	603	49.8	603	22	AAH68381		C glutamicum codin
	4	603	49.8	603	25	ACA01297		C. glutamicum deri
c	5	449	37.1	1185	22	AAH68383		C glutamicum codin
	6	197	16.3	951	22	AAH68382		C glutamicum codin
	7	197	16.3	951	25	ACA01298		C. glutamicum deri
	8	79	6.5	1377	24	ABN89593		Mycobacterium lepr
	9	79	6.5	4922	24	ABN89585		Phaseolin promoter
	10	75	6.2	4403765	22	AAI99683		Mycobacterium tube
	11	75	6.2	4411529	22	AAI99682		Mycobacterium tube
c	12	72.6	6.0	49617	22	AAF28541		Genomic fragment #
c	13	71.8	5.9	2944528	24	ABA03041		Listeria monocytog
	14	71	5.9	3075	22	AAF72006		Corynebacterium gl
	15	71	5.9	3075	22	AAF72049		Corynebacterium gl
c	16	68.6	5.7	977	24	ABQ70456		Listeria monocytog
c	17	63.6	5.3	5998	20	AAX13056		Enterococcus faeca
c	18	63.6	5.3	5998	24	ABS98851		Enterococcus faeca
	19	62.8	5.2	1932	21	AAC62474		E. coli NADPH-thio
	20	62.2	5.1	311	24	ABK78994		Bacillus clausii g
	21	61.2	5.1	264	24	ABN93197		Staphylococcus epi
	22	61.2	5.1	336	22	AAH53675		S. epidermidis ope
	23	61.2	5.1	933	20	AAZ21081		Staphylococcus epi
	24	61.2	5.1	933	22	AAH52874		S. epidermidis ope
c	25	61.2	5.1	2987	22	AAH55003		S. epidermidis gen
c	26	61.2	5.1	3284	22	AAH54795		S. epidermidis gen
c	27	61.2	5.1	3431	22	AAH55071		S. epidermidis gen
	28	61.2	5.1	3931	22	AAH54044		S. epidermidis gen
	29	61	5.0	2365589	24	ABA90521		Genomic sequence o
	30	60.8	5.0	1608	24	ABZ14517		Arabidopsis thalia
	31	60.2	5.0	966	24	ABN89590		Escherichia coli t
c	32	59.6	4.9	50925	21	AAA81487		N. meningitidis pa
c	33	59.6	4.9	349980	21	AAF21610		Neisseria meningit
c	34	59.6	4.9	1437668	21	AAA81490		N. meningitidis B
c	35	59.2	4.9	349980	24	ABQ81845		Bifidobacterium lo
	36	58.8	4.9	684707	24	ABQ67196		Listeria innocua c
c	37	58.8	4.9	3011208	24	ABQ69245		Listeria innocua D
	38	58	4.8	948	25	ABZ39725		N. gonorrhoeae nuc
c	39	57.8	4.8	1002	23	AAS93914		DNA encoding novel
	40	57.8	4.8	1002	23	AAS94482		DNA encoding novel
	41	56.4	4.7	936	20	AAZ21080		Staphylococcus aur
	42	56.4	4.7	936	22	AAS00195		S. aureus DNA enco
	43	56.4	4.7	13086	18	AAV74327		Staphylococcus aur
c	44	55	4.5	1286	23	ABK43473		DNA encoding novel
	45	55	4.5	3822	23	AAS94485		DNA encoding novel

ALIGNMENTS

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OM nucleic - nucleic search, using sw model

Run on: September 21, 2003, 16:22:51 ; Search time 2883 Seconds
                                               (without alignments)
                                               10209.060 Million cell updates/sec

Title: US-09-942-935-1
Perfect score: 1211
Sequence: 1 gacaccaatccacagatgca..........ccaggctttgaaaagggaat 1211

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
                 1:   em_estba:*
                 2:   em_esthum:*
                 3:   em_estin:*
                 4:   em_estmu:*
                 5:   em_estov:*
                 6:   em_estpl:*
                 7:   em_estro:*
                 8:   em_htc:*
                 9:   gb_est1:*
                 10: gb_est2:*
                 11: gb_htc:*
                 12: gb_est3:*
                 13: gb_est4:*
                 14: gb_est5:*
                 15: em_estfun:*
                 16: em_estom:*
                 17: em_gss_hum:*
                 18: em_gss_inv:*
                 19: em_gss_pln:*
                 20: em_gss_vrt:*
                 21: em_gss_fun:*
                 22: em_gss_mam:*
                 23: em_gss_mus:*
                 24: em_gss_pro:*
                 25: em_gss_rod:*
                 26: em_gss_phg:*
                 27: em_gss_vrl:*
                 28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	75.2	6.2	789	14	CD576244	CD576244 UCRPT01_0
2	72.4	6.0	646	12	BI096251	BI096251 S1D_F05_S
3	72.2	6.0	535	9	AV628023	AV628023 AV628023
4	68.6	5.7	721	13	BQ862556	BQ862556 QGC21G18.
5	67.4	5.6	755	13	BQ863331	BQ863331 QGC23J12.
6	64.4	5.3	483	13	BQ595059	BQ595059 E012711-0
7	63	5.2	623	14	CA839585	CA839585 MCT029B08
8	63	5.2	664	14	CA840153	CA840153 MCT040C12
9	61	5.0	490	10	BE321389	BE321389 NF024C10I
10	61	5.0	523	10	BE321441	BE321441 NF025C10I
11	61	5.0	593	10	BG452377	BG452377 NF085C09L
12	61	5.0	609	10	BG451523	BG451523 NF110B04D
13	61	5.0	655	10	BF650364	BF650364 NF096A12E
14	61	5.0	659	10	BF636499	BF636499 NF091G04D
15	61	5.0	662	10	BE322274	BE322274 NF022E01I
16	61	5.0	663	9	AW692011	AW692011 NF046F03S
17	61	5.0	666	13	BQ139032	BQ139032 NF010C06P
18	61	5.0	667	13	BQ138990	BQ138990 NF009H09P
19	61	5.0	671	10	BG449209	BG449209 NF043G10I
20	61	5.0	692	10	BF520046	BF520046 EST457514
21	60.8	5.0	563	9	AW030413	AW030413 EST273668
22	60.8	5.0	564	10	BE449605	BE449605 EST356364
23	60.8	5.0	590	9	AV828748	AV828748 AV828748
24	60.2	5.0	592	12	BJ073890	BJ073890 BJ073890
25	60	5.0	504	10	BE321909	BE321909 NF045F02I
c 26	60	5.0	571	9	AW650215	AW650215 EST328669
27	59.2	4.9	345	10	BE920457	BE920457 EST424226
28	59.2	4.9	521	10	BG589427	BG589427 EST497269
29	59.2	4.9	531	10	BE920949	BE920949 EST424718
30	59.2	4.9	756	10	BG600533	BG600533 EST505428
31	59	4.9	582	14	CA655448	CA655448 wlm0.pk00
32	57.8	4.8	615	12	BQ045955	BQ045955 EST595073
33	57.2	4.7	240	9	AV628019	AV628019 AV628019
34	56.6	4.7	446	9	AV631626	AV631626 AV631626
35	55	4.5	471	12	BI943760	BI943760 sa35d07.y
36	55	4.5	600	12	BI946183	BI946183 sv13d08.y
c 37	54.6	4.5	706	14	CA918869	CA918869 EST636587
38	54.2	4.5	907	29	BZ555070	BZ555070 pacs1-60_
39	53.8	4.4	831	14	CB676820	CB676820 OSJNEe13E
c 40	53.6	4.4	524	29	CC338816	CC338816 OGUAO91TV
c 41	53.6	4.4	597	29	CC330971	CC330971 OGSAB30TV
42	53.6	4.4	610	29	CC336857	CC336857 OGUAO91TH
c 43	53.4	4.4	613	28	BH879728	BH879728 ht48d06.b
44	52.8	4.4	436	10	BE922916	BE922916 EST426685
45	52.6	4.3	499	10	BG739547	BG739547 EM1_82_C0

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OM nucleic - nucleic search, using sw model

Run on: September 21, 2003, 16:24:01 ; Search time 91 Seconds
                                     (without alignments)
                                     5873.791 Million cell updates/sec

Title: US-09-942-935-1
Perfect score: 1211
Sequence: 1 gacaccaatccacagatgca..........ccaggctttgaaaagggaat 1211

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_NA:*
               1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
               2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
               3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
               4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
               5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
               6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                             SUMMARIES
                     %
Result   Query
    No.   Score   Match Length DB   ID   Description
----
c   1   79.6   6.6   1443   4   US-09-221-017B-685   Sequence 685, App
    2   75   6.2 4403765   3   US-09-103-840A-2   Sequence 2, Appli
    3   75   6.2 4411529   3   US-09-103-840A-1   Sequence 1, Appli
    4   63.2   5.2   600   4   US-09-252-991A-14870   Sequence 14870, A
c   5   63.2   5.2   666   4   US-09-252-991A-14492   Sequence 14492, A
    6   62.6   5.2   972   4   US-09-252-991A-13278   Sequence 13278, A
c   7   62.6   5.2   1413   4   US-09-252-991A-12680   Sequence 12680, A
    8   61.2   5.1   264   4   US-09-134-001C-2660   Sequence 2660, Ap
    9   60.2   5.0   966   4   US-09-540-014-27   Sequence 27, Appl
    10   55   4.5   954   4   US-09-328-352-3988   Sequence 3988, Ap
c   11   51.8   4.3 1830121   4   US-09-557-884-1   Sequence 1, Appli

OM nucleic - nucleic search, using sw model

Run on: September 21, 2003, 18:35:57 ; Search time 340 Seconds
                                              (without alignments)
                                              8761.649 Million cell updates/sec

Title: US-09-942-935-1
Perfect score: 1211
Sequence: 1 gacaccaatccacagatgca..........ccaggctttgaaaagggaat 1211

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 1660708 seqs, 1229959015 residues

Total number of hits satisfying chosen parameters: 3321416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA:*
        1:   /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
        2:   /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
        3:   /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
        4:   /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
        5:   /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
        6:   /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
        7:   /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
        8:   /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
        9:   /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
        10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
        11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
        12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
        13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
        14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
        15: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
        16: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
        17: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

```
                              SUMMARIES
                         %
       Result           Query
         No.   Score   Match Length DB  ID                         Description
       ------------------------------------------------------------------------------
          1   1211   100.0    1211  10  US-09-942-935-1            Sequence 1, Appli
          2   1211   100.0 3309400  10  US-09-738-626-1  Nakagawa  Sequence 1, Appli
          3    603    49.8     603  10  US-09-738-626-3416         Sequence 3416, Ap
  c       4    449    37.1    1185  10  US-09-738-626-3418         Sequence 3418, Ap
          5    197    16.3     951  10  US-09-738-626-3417         Sequence 3417, Ap
          6     79     6.5    1377  12  US-10-032-201B-50          Sequence 50, Appl
          7     79     6.5    4922  12  US-10-032-201B-30          Sequence 30, Appl
  c       8   63.6     5.3    5998  10  US-09-070-927A-119         Sequence 119, App
          9   62.2     5.1     311  10  US-09-974-300-6285         Sequence 6285, Ap
         10   60.8     5.0    1608  10  US-09-938-842A-2322        Sequence 2322, Ap
         11   60.4     5.0     969  14  US-10-156-761-4289         Sequence 4289, Ap
         12   60.4     5.0 9025608  14  US-10-156-761-1            Sequence 1, Appli
         13   60.2     5.0     966  12  US-10-091-841-27           Sequence 27, Appl
         14   60.2     5.0     966  12  US-10-032-201B-44          Sequence 44, Appl
         15   56.4     4.7     936  10  US-09-925-637-13           Sequence 13, Appl
         16   56.4     4.7     936  14  US-10-084-205-13           Sequence 13, Appl
         17   56.4     4.7   13086   8  US-08-781-986A-16          Sequence 16, Appl
         18     55     4.5     711  14  US-10-156-761-4287         Sequence 4287, Ap
  c      19   51.8     4.3 1830121  14  US-10-329-960-1            Sequence 1, Appli
         20   51.2     4.2   19024  10  US-09-070-927A-179         Sequence 179, App
         21   51.2     4.2  640681  10  US-09-790-988-1            Sequence 1, Appli
         22   50.6     4.2    1021  12  US-10-306-292-24           Sequence 24, Appl
         23     48     4.0    3249  10  US-09-738-626-3414         Sequence 3414, Ap
         24   47.4     3.9     995  12  US-10-091-841-10           Sequence 10, Appl
         25   47.4     3.9     995  12  US-10-091-841-23           Sequence 23, Appl
         26   45.4     3.7     579  10  US-09-738-626-284          Sequence 284, App
         27   45.4     3.7    1109  10  US-09-941-936A-1           Sequence 1, Appli
  c      28   45.4     3.7 3309400  10  US-09-738-626-1            Sequence 1, Appli
         29     43     3.6    1560  12  US-10-306-292-26           Sequence 26, Appl
         30   42.4     3.5     912  10  US-09-974-300-1977         Sequence 1977, Ap
         31   42.2     3.5    1330  10  US-09-935-757-1            Sequence 1, Appli
         32   42.2     3.5    2086  10  US-09-935-757-5            Sequence 5, Appli
         33     42     3.5    1848  14  US-10-156-761-7222         Sequence 7222, Ap
  c      34   41.2     3.4     837  14  US-10-184-644-454          Sequence 454, App
  c      35   41.2     3.4     837  14  US-10-184-634-454          Sequence 454, App
         36   40.8     3.4   10809  12  US-09-960-858-7            Sequence 7, Appli
         37   40.8     3.4   10809  12  US-09-960-870-7            Sequence 7, Appli
         38   40.2     3.3     639  10  US-09-738-626-1241         Sequence 1241, Ap
         39     40     3.3    1122  14  US-10-128-714-7016         Sequence 7016, Ap
         40   37.8     3.1  580073  12  US-10-205-220-1            Sequence 1, Appli
         41   37.6     3.1    1518  10  US-09-738-626-208          Sequence 208, App
         42   37.4     3.1    1272  14  US-10-128-714-6016         Sequence 6016, Ap
         43   37.4     3.1    2966  14  US-10-128-714-16           Sequence 16, Appl
         44   37.4     3.1    3272  14  US-10-128-714-5016         Sequence 5016, Ap
         45   37.2     3.1     240   9  US-09-294-093B-4182        Sequence 4182, Ap
```

                              ALIGNMENTS

RESULT 1
US-09-942-935-1

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OM nucleic - nucleic search, using sw model

Run on: September 21, 2003, 19:47:42 ; Search time 4589 Seconds
                                            (without alignments)
                                            10795.720 Million cell updates/sec

Title: US-09-942-935-1
Perfect score: 1211
Sequence: 1 gacaccaatccacagatgca..........ccaggctttgaaaagggaat 1211

Scoring table: OLIGO_NUC
                 Gapop 60.0 , Gapext 60.0

Searched: 2888711 seqs, 20454813386 residues

Word size :   0

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :   GenEmbl:*
                 1: gb_ba:*
                 2: gb_htg:*
                 3: gb_in:*
                 4: gb_om:*
                 5: gb_ov:*
                 6: gb_pat:*
                 7: gb_ph:*
                 8: gb_pl:*
                 9: gb_pr:*
                 10: gb_ro:*
                 11: gb_sts:*
                 12: gb_sy:*
                 13: gb_un:*
                 14: gb_vi:*
                 15: em_ba:*
                 16: em_fun:*
                 17: em_hum:*
                 18: em_in:*
                 19: em_mu:*
                 20: em_om:*
                 21: em_or:*
                 22: em_ov:*
                 23: em_pat:*
                 24: em_ph:*
                 25: em_pl:*
                 26: em_ro:*
                 27: em_sts:*

```
28:  em_un:*
29:  em_vi:*
30:  em_htg_hum:*
31:  em_htg_inv:*
32:  em_htg_other:*
33:  em_htg_mus:*
34:  em_htg_pln:*
35:  em_htg_rod:*
36:  em_htg_mam:*
37:  em_htg_vrt:*
38:  em_sy:*
39:  em_htgo_hum:*
40:  em_htgo_mus:*
41:  em_htgo_other:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID		Description
1	1211	100.0	1211	6	AX394331	*Appl. WO*	AX394331 Sequence
2	1211	100.0	309400	6	AX127153	*EP 1108790*	AX127153 Sequence
3	1211	100.0	325651	1	AP005283	*GenBank AP005283*	AP005283 Corynebac
4	603	49.8	603	6	AX123500		AX123500 Sequence
5	603	49.8	603	6	BD165617		BD165617 Novel pol
c 6	449	37.1	1185	6	AX123502		AX123502 Sequence
c 7	449	37.1	1185	6	BD165619		BD165619 Novel pol
8	197	16.3	951	6	AX123501		AX123501 Sequence
9	197	16.3	951	6	BD165618		BD165618 Novel pol
10	71	5.9	3075	6	AX064225	*Pompejus WO 0100893*	AX064225 Sequence
11	71	5.9	3075	6	AX064311		AX064311 Sequence
12	48	4.0	3249	6	AX123498		AX123498 Sequence
13	48	4.0	3249	6	BD165615		BD165615 Novel pol
c 14	22	1.8	191301	2	BX323582		BX323582 Danio rer
c 15	21	1.7	3506	6	AX319470		AX319470 Sequence
16	21	1.7	144699	2	AC125881		AC125881 Rattus no
c 17	21	1.7	153841	2	AC091527		AC091527 Trypanoso
18	21	1.7	157848	10	AC091712		AC091712 Rattus no
19	21	1.7	168843	2	AC091711		AC091711 Rattus no
c 20	21	1.7	196904	2	AC113217		AC113217 Rattus no
c 21	21	1.7	211624	10	AC114817		AC114817 Mus muscu
22	21	1.7	242400	2	AC096829		AC096829 Rattus no
23	21	1.7	247946	2	AC133092		AC133092 Mus muscu
24	21	1.7	252376	2	AC105580		AC105580 Rattus no
c 25	21	1.7	271432	2	AC095563		AC095563 Rattus no
26	20	1.7	1302	6	AX413806		AX413806 Sequence
27	20	1.7	2734	8	ARU421692		AJ421692 Anaptychi
c 28	20	1.7	3010	1	AF105341		AF105341 Listeria
c 29	20	1.7	37533	3	CBRG36C02		AC084560 Caenorhab
c 30	20	1.7	75650	2	AC018145		AC018145 Drosophil
31	20	1.7	87340	1	AP005224		AP005224 Corynebac
32	20	1.7	102842	10	AL671903		AL671903 Mouse DNA
c 33	20	1.7	105466	2	AL356281		AL356281 Homo sapi

```
                        GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on:          September 21, 2003, 18:38:12 ; Search time 390 Seconds
                                        (without alignments)
                                        8382.101 Million cell updates/sec


Title:           US-09-942-935-1
Perfect score:   1211
Sequence:        1 gacaccaatccacagatgca..........ccaggctttgaaaagggaat 1211


Scoring table:   OLIGO_NUC
                 Gapop 60.0 , Gapext 60.0


Searched:        2552756 seqs, 1349719017 residues


Word size :      0


Total number of hits satisfying chosen parameters:      5105512


Minimum DB seq length: 0
Maximum DB seq length: 2000000000


Post-processing: Listing first 45 summaries


Database :       N_Geneseq_19Jun03:*
                 1:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
                 2:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
                 3:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
                 4:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
                 5:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
                 6:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
                 7:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
                 8:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
                 9:  /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
                 10: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*
                 11: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
                 12: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
                 13: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
                 14: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
                 15: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
                 16: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
                 17: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
                 18: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*
                 19: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
                 20: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
                 21: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
                 22: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
                 23: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
                 24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
                 25: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2003.DAT:*

       Pred. No. is the number of results predicted by chance to have a
       score greater than or equal to the score of the result being printed,
```

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID		Description
1	1211	100.0	1211	24	AAL42355		Corynebacterium gl
2	1211	100.0	309400	22	AAH68534	*Nakagawa*	C glutamicum codin
3	603	49.8	603	22	AAH68381		C glutamicum codin
4	603	49.8	603	25	ACA01297		C. glutamicum deri
c 5	449	37.1	1185	22	AAH68383		C glutamicum codin
6	197	16.3	951	22	AAH68382		C glutamicum codin
7	197	16.3	951	25	ACA01298		C. glutamicum deri
8	71	5.9	3075	22	AAF72006	*Pompejus*	Corynebacterium gl
9	71	5.9	3075	22	AAF72049		Corynebacterium gl
10	48	4.0	3249	22	AAH68379		C glutamicum codin
c 11	21	1.7	3506	24	AAI64198		Rat CRF2alpha rece
12	20	1.7	28	24	AAL42358		Corynebacterium gl
c 13	20	1.7	28	24	AAL42359		Corynebacterium gl
14	20	1.7	1302	24	ABQ67984		Listeria monocytog
c 15	20	1.7	4801	23	ABL23188		Drosophila melanog
16	20	1.7	198161	24	ABK83564		Human cDNA differe
c 17	20	1.7	2944528	24	ABA03041		Listeria monocytog
c 18	19	1.6	1709	18	AAT84145		DNA encoding one u
c 19	19	1.6	1709	19	AAV53488		DNA encoding a X-P
c 20	19	1.6	2567	23	ABL21964		Drosophila melanog
21	19	1.6	6378	24	ABQ67027		Human angiogenesis
22	19	1.6	6378	24	ABL32176		Human immune syste
23	19	1.6	69936	21	AAA81479		N. meningitidis pa
c 24	19	1.6	349980	21	AAF21607		Neisseria meningit
c 25	19	1.6	1437668	21	AAA81490		N. meningitidis B
26	18	1.5	383	21	AAC28072		Human secreted pro
c 27	18	1.5	609	23	ABV49963		Human prostate exp
28	18	1.5	860	24	ABQ52662		Oligonucleotide fo
c 29	18	1.5	860	24	ABQ52663		Oligonucleotide fo
30	18	1.5	1000	24	ABQ74939		Mouse bHLH transcr
31	18	1.5	1052	21	AAC47957		Arabidopsis thalia
32	18	1.5	1128	21	AAC44002		Arabidopsis thalia
33	18	1.5	1234	24	ABQ41370		Oligonucleotide fo
c 34	18	1.5	1234	24	ABQ41371		Oligonucleotide fo
35	18	1.5	1933	17	AAT43282		Coding sequence fo
36	18	1.5	2069	15	AAQ77860		ATP-sensitive K ch
37	18	1.5	2644	23	ABL09867		Drosophila melanog
38	18	1.5	6020	24	ABN79993		Human chemically m
39	18	1.5	6096	23	ABL09866		Drosophila melanog
c 40	18	1.5	6170	24	ABQ93471		Human cDNA SEQ ID
c 41	18	1.5	7369	25	ABZ09879		Human 5' and/or re
42	18	1.5	10207	24	ABQ74941		Mouse bHLH transcr
c 43	18	1.5	11460	24	AAD38805		CODR1 ORF from ric
44	18	1.5	16738	22	AAK70864		Human immune/haema
45	18	1.5	69300	24	AAD38804		BAC clone E2P5 fro

ALIGNMENTS

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OM nucleic - nucleic search, using sw model

Run on: September 21, 2003, 19:50:52 ; Search time 2884 Seconds
                                              (without alignments)
                                   10205.520 Million cell updates/sec

Title: US-09-942-935-1
Perfect score: 1211
Sequence: 1 gacaccaatccacagatgca..........ccaggctttgaaaagggaat 1211

Scoring table: OL1GO_NUC
                Gapop 60.0 , Gapext 60.0

Searched: 22781392 seqs, 12152238056 residues

Word size :   0

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :   EST:*
                1: em_estba:*
                2: em_esthum:*
                3: em_estin:*
                4: em_estmu:*
                5: em_estov:*
                6: em_estpl:*
                7: em_estro:*
                8: em_htc:*
                9: gb_est1:*
                10: gb_est2:*
                11: gb_htc:*
                12: gb_est3:*
                13: gb_est4:*
                14: gb_est5:*
                15: em_estfun:*
                16: em_estom:*
                17: em_gss_hum:*
                18: em_gss_inv:*
                19: em_gss_pln:*
                20: em_gss_vrt:*
                21: em_gss_fun:*
                22: em_gss_mam:*
                23: em_gss_mus:*
                24: em_gss_pro:*
                25: em_gss_rod:*
                26: em_gss_phg:*
                27: em_gss_vrl:*
                28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	22	1.8	618	10	BG656707	BG656707 df47b06.y
c	2	22	1.8	852	14	CD252970	CD252970 AGENCOURT
c	3	21	1.7	358	29	TA58F03Q	AL455737 T. brucei
	4	21	1.7	558	28	AZ387580	AZ387580 1M0147G09
c	5	20	1.7	479	28	AZ552929	AZ552929 RPCI-23-1
c	6	20	1.7	636	28	AZ241095	AZ241095 RPCI-23-3
	7	20	1.7	794	9	AI439244	AI439244 ti59a03.x
	8	20	1.7	971	10	BG393115	BG393115 602411384
	9	19	1.6	285	29	CC112112	CC112112 NDL.23C11
	10	19	1.6	290	29	CC142352	CC142352 NDL.69F6.
c	11	19	1.6	300	9	AU231710	AU231710 AU231710
	12	19	1.6	308	29	CC013856	CC013856 PUEBF69TD
	13	19	1.6	317	10	BE364026	BE364026 PI1_11_F0
	14	19	1.6	380	28	BH877108	BH877108 hr35e11.b
	15	19	1.6	387	29	BZ331847	BZ331847 hx23d03.g
	16	19	1.6	411	29	BZ648869	BZ648869 OGAOP23TC
	17	19	1.6	419	12	BP099919	BP099919 BP099919
c	18	19	1.6	428	29	BZ346375	BZ346375 hv18b09.b
	19	19	1.6	442	14	CD003371	CD003371 EST1504 N
c	20	19	1.6	445	28	BH127538	BH127538 G-1h21.f
	21	19	1.6	452	28	BH710348	BH710348 BOMBV59TF
	22	19	1.6	460	28	AZ696294	AZ696294 RPCI-23-2
	23	19	1.6	465	28	BH869577	BH869577 hl45f07.g
	24	19	1.6	478	12	BI419494	BI419494 LjNEST40f
c	25	19	1.6	486	28	AQ934851	AQ934851 RPCI-23-2
	26	19	1.6	490	29	CC156727	CC156727 ig15b10.b
	27	19	1.6	503	29	BZ315255	BZ315255 ia56f04.b
	28	19	1.6	524	29	BZ333551	BZ333551 hx70h12.g
c	29	19	1.6	527	13	BQ588119	BQ588119 E012337-0
	30	19	1.6	539	29	CC166564	CC166564 ii54h04.b
	31	19	1.6	547	29	BZ309344	BZ309344 ic06a10.b
	32	19	1.6	556	29	PT022K05R	AL446773 Parameciu
c	33	19	1.6	559	29	CNS02DIZ	AL192500 Tetraodon
	34	19	1.6	560	29	BZ336835	BZ336835 hz39e06.b
	35	19	1.6	561	29	BZ628389	BZ628389 ih59h05.g
	36	19	1.6	578	29	BZ305613	BZ305613 hw56b06.b
	37	19	1.6	584	14	CA035588	CA035588 4001314 B
c	38	19	1.6	585	28	BZ165599	BZ165599 CH230-277
c	39	19	1.6	588	29	BZ648875	BZ648875 OGAOP23TM
c	40	19	1.6	589	29	BZ331908	BZ331908 hx23h11.g
c	41	19	1.6	590	28	AQ753987	AQ753987 HS_5395_B
c	42	19	1.6	591	29	PT017E15U	AL447151 Parameciu
	43	19	1.6	593	29	BZ347262	BZ347262 ic82c03.b
	44	19	1.6	596	28	AZ078139	AZ078139 RPCI-23-4
c	45	19	1.6	606	28	AQ524534	AQ524534 HS_5199_A

```
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OM nucleic - nucleic search, using sw model

Run on:          September 21, 2003, 22:08:32 ; Search time 340 Seconds
                                            (without alignments)
                                            8761.649 Million cell updates/sec


Title:           US-09-942-935-1
Perfect score:   1211
Sequence:        1 gacaccaatccacagatgca..........ccaggctttgaaaagggaat 1211


Scoring table:   OLIGO_NUC
                 Gapop 60.0 , Gapext 60.0


Searched:        1660708 seqs, 1229959015 residues


Word size :      0


Total number of hits satisfying chosen parameters:      3321416


Minimum DB seq length: 0
Maximum DB seq length: 2000000000


Post-processing: Listing first 45 summaries


Database :       Published_Applications_NA:*
                 1:  /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
                 2:  /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
                 3:  /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
                 4:  /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
                 5:  /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
                 6:  /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
                 7:  /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
                 8:  /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
                 9:  /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
                 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
                 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
                 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
                 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
                 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
                 15: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
                 16: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
                 17: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.
```

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1211	100.0	1211	10	US-09-942-935-1	Sequence 1, Appli
	2	1211	100.0	3309400	10	US-09-738-626-1	Sequence 1, Appli
	3	603	49.8	603	10	US-09-738-626-3416	Sequence 3416, Ap
c	4	449	37.1	1185	10	US-09-738-626-3418	Sequence 3418, Ap
	5	197	16.3	951	10	US-09-738-626-3417	Sequence 3417, Ap
	6	48	4.0	3249	10	US-09-738-626-3414	Sequence 3414, Ap
c	7	21	1.7	3506	9	US-09-847-852-1	Sequence 1, Appli
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c	9	19	1.6	300	14	US-10-156-761-1964	Sequence 1964, Ap
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	11	19	1.6	6378	12	US-10-311-455-149	Sequence 149, App
	12	19	1.6	9025608	14	US-10-156-761-1	Sequence 1, Appli
c	13	18	1.5	434	13	US-10-027-632-86208	Sequence 86208, A
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c	15	18	1.5	567	14	US-10-156-761-5054	Sequence 5054, Ap
c	16	18	1.5	648	13	US-10-027-632-8947	Sequence 8947, Ap
c	17	18	1.5	678	13	US-10-027-632-273855	Sequence 273855,
	18	18	1.5	749	13	US-10-027-632-11318	Sequence 11318, A
	19	18	1.5	749	13	US-10-027-632-11319	Sequence 11319, A
c	20	18	1.5	2000	10	US-09-887-576-852	Sequence 852, App
c	21	18	1.5	119596	14	US-10-270-336-3	Sequence 3, Appli
c	22	17	1.4	116	10	US-09-966-880A-14	Sequence 14, Appl
c	23	17	1.4	120	10	US-09-969-373-1351	Sequence 1351, Ap
	24	17	1.4	173	9	US-09-864-761-26899	Sequence 26899, A
c	25	17	1.4	243	10	US-09-878-574-10603	Sequence 10603, A
c	26	17	1.4	389	10	US-09-783-590-10879	Sequence 10879, A
	27	17	1.4	407	13	US-10-027-632-74758	Sequence 74758, A
c	28	17	1.4	456	9	US-09-770-444-540	Sequence 540, App
	29	17	1.4	458	9	US-09-864-761-10264	Sequence 10264, A
	30	17	1.4	458	9	US-09-864-761-14121	Sequence 14121, A
c	31	17	1.4	465	13	US-10-027-632-20382	Sequence 20382, A
c	32	17	1.4	479	10	US-09-924-035A-158	Sequence 158, App
	33	17	1.4	479	13	US-10-027-632-53238	Sequence 53238, A
c	34	17	1.4	539	10	US-09-321-801-18	Sequence 18, Appl
	35	17	1.4	542	14	US-10-106-698-4281	Sequence 4281, Ap
	36	17	1.4	559	13	US-10-027-632-39555	Sequence 39555, A
	37	17	1.4	565	13	US-10-027-632-80791	Sequence 80791, A
	38	17	1.4	565	13	US-10-027-632-109721	Sequence 109721,
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	41	17	1.4	585	13	US-10-027-632-207083	Sequence 207083,
	42	17	1.4	589	13	US-10-027-632-73937	Sequence 73937, A
c	43	17	1.4	602	13	US-10-027-632-275824	Sequence 275824,
	44	17	1.4	609	13	US-10-027-632-205007	Sequence 205007,
c	45	17	1.4	614	13	US-10-027-632-227649	Sequence 227649,

ALIGNMENTS

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US-09-942-935-1

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OM nucleic - nucleic search, using sw model

Run on: September 21, 2003, 19:57:12 ; Search time 92 Seconds
                                          (without alignments)
                                          5809.945 Million cell updates/sec

Title: US-09-942-935-1
Perfect score: 1211
Sequence: 1 gacaccaatccacagatgca..........ccaggctttgaaaagggaat 1211

Scoring table: OLIGO_NUC
                 Gapop 60.0 , Gapext 60.0

Searched: 569978 seqs, 220691566 residues

Word size :   0

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :   Issued_Patents_NA:*
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        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                       %
Result   Query
    No.   Score   Match Length DB   ID   Description
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  c   1   19   1.6   963   4   US-09-252-991A-2989   Sequence 2989, Ap
      2   19   1.6   1431   4   US-09-252-991A-2787   Sequence 2787, Ap
  c   3   19   1.6   1707   4   US-09-252-991A-3180   Sequence 3180, Ap
  c   4   19   1.6   1709   4   US-08-936-165A-188   Sequence 188, App
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  c   6   18   1.5 1230025   4   US-09-198-452A-1   Sequence 1, Appli
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  c   8   17   1.4   404   3   US-09-174-437-33   Sequence 33, Appl
  c   9   17   1.4   404   4   US-09-686-055A-33   Sequence 33, Appl
     10   17   1.4   495   4   US-09-252-991A-15616   Sequence 15616, A
  c 11   17   1.4   528   2   US-08-687-080-83   Sequence 83, Appl